1600

RAW SEQUENCE LISTING   DATE: 05/07/2003
PATENT APPLICATION: US/09/880,821A   TIME: 12:18:06

Input Set : **A:\EP.txt**
Output Set: **N:\CRF4\05072003\I880821A.raw**

```
   5 <110> APPLICANT: EAGLES, Peter Anthony Minter
   7        ZHENG, Richard Qihao
   9        BTG INTERNATIONAL LIMITED
  13 <120> TITLE OF INVENTION: RIBOZYMAL NUCLEIC ACID
  17 <130> FILE REFERENCE: PF 137 765 WO/RKP
C--> 21 <140> CURRENT APPLICATION NUMBER: US/09/880,821A
C--> 23 <141> CURRENT FILING DATE: 2001-06-15
  27 <150> PRIOR APPLICATION NUMBER: GB 9800870.9
  29 <151> PRIOR FILING DATE: 1998-01-15
  33 <150> PRIOR APPLICATION NUMBER: GB 9824794.3
  35 <151> PRIOR FILING DATE: 1998-12-23
  39 <160> NUMBER OF SEQ ID NOS: 15
  43 <170> SOFTWARE: PatentIn Ver. 2.0
```

[handwritten: pp 1-4]
[handwritten: Does Not Comply Corrected Diskette Needed]

ERRORED SEQUENCES

```
 323 <210> SEQ ID NO: 14
 325 <211> LENGTH: 93
 327 <212> TYPE: DNA
 329 <213> ORGANISM: Artificial Sequence
 333 <220> FEATURE:
W--> 335 <223> OTHER INFORMATION:
W--> 335 <400>14
E--> 336 gggcgaaagc ccuagauugc ugaugagcgc gaaagcgcga aacuuguccu  cuacgaaagu
E--> 338 agagcugaug aaccgaaag gucgaaacaa gug
 341 <210> SEQ ID NO: 15
 343 <211> LENGTH: 100
 345 <212> TYPE: DNA
 347 <213> ORGANISM: Artificial Sequence
 351 <220> FEATURE:
W--> 353 <223> OTHER INFORMATION:
W--> 353 <400>15
E--> 354 gggccgaaag gccccucacu cugaugagcg cgaaagcgcg aaacguuguc cucugagaaa
 356 ucagagcuga ugagguccga aaggaccgaa acaacguuuc
```

[handwritten annotations: "92 shown" (near line 325), "see p. 4 for error explanation", "Per 1.822 of sequence rules, insert cumulative base total at right margin 60 of each line", "92 93", "group of 9 (one missing)", "see p.4", "60 insert 100", "see pp 2-3 for more errors"]

<210> 1

<211> 13

<212> RNA   *invalid <213> response*

<213> (CD4-positive T cell, CCR5 receptor)

see item 10 on Erm Summary Sheet

<400> 1

The [...] shown exist throughout
the [...] Please check subsequent
sequ[...] [...]lar errors.

<210> 13

<211> 48

<212> DNA

see p.4

<213> Artificial Sequence

<220>

<400>13
gggcgaaagc cucagauugc ugaugagcgc gaaagcggca aacuuguc

48

48 (see item 1 on Error Summary Sheet)

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 05/07/2003
PATENT APPLICATION: US/09/880,821A   TIME: 12:18:07

Input Set : **A:\EP.txt**
Output Set: **N:\CRF4\05072003\I880821A.raw**

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 3,5,7,9,11,13,15,17,19,21,23,25,27,29,31,33,35,37,39,41,43
Seq#:1; Line(s) 45,47,49,51,53,55,57,59,61,63
Seq#:2; Line(s) 65,67,69,71,73,75,77,79
Seq#:3; Line(s) 81,83,85,87,89,91,93,95
Seq#:4; Line(s) 97,99,101,103,105,107,109,111
Seq#:5; Line(s) 113,115,117,119,121,123,125,127,129,131,133,135,137,139,141
Seq#:6; Line(s) 143,145,147,149,151,153,155,157,159
Seq#:7; Line(s) 161,163,165,167,169,171,173,175,177
Seq#:8; Line(s) 179,181,183,185,187,189,191,193,195,197,199,201,203,205,207
Seq#:9; Line(s) 209,211,213,215,217,219,221,223,225,227,229,231
Seq#:10; Line(s) 233,235,237,239,241,243,245,247,249,251,253,255
Seq#:11; Line(s) 257,259,261,263,265,267,269,271,273,275,277,279,281
Seq#:12; Line(s) 283,285,287,289,291,293,295,297,299,301,303,305,307,308
Seq#:13; Line(s) 310,312,314,316,318,321,323
Seq#:14; Line(s) 325,327,329,331,333,338,341
Seq#:15; Line(s) 343,345,347,349,351

Use of <220> Feature(NEW RULES):
Sequence(s)__are missing the <220> Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence"
or"Unknown". Please explain source of genetic material in <220> to <223>
section (See "Federal Register," 6/01/98, Vol. 63, No. 104,pp.29631-32)
(Sec.1.823 of new Rules)

Seq#:13,14,15   *error explanation*

Input Set : **A:\EP.txt**
Output Set: **N:\CRF4\05072003\I880821A.raw**

L:21 M:270 C: Current Application Number differs, Replaced Application Number
L:23 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:320 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:13, <213>
ORGANISM:Artificial Sequence
L:320 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13,Line#:320
L:335 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:14, <213>
ORGANISM:Artificial Sequence
L:335 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:14,Line#:335
L:336 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:14
M:254 Repeated in SeqNo=14
L:338 M:252 E: No. of Seq. differs, <211> LENGTH:Input:93 Found:92 SEQ:14
L:353 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:15, <213>
ORGANISM:Artificial Sequence
L:353 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:353
L:354 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:15

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

☐ 7. Other: _____

Applicant Must Provide:

☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".

☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
PatentIn Software Program Support (SIRA)
    Technical Assistance...703-287-0200
    To Purchase PatentIn Software.......................703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/880, 821A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ___ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ___ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ___ Misaligned Amino Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ___ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 ___ Variable Length

Sequence(s) ___ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ___ PatentIn 2.0 "bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) ___. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 ___ Skipped Sequences (OLD RULES)

Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ___ Skipped Sequences (NEW RULES)

Sequence(s) ___ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ___ Use of n's or Xaa's (NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ___ Invalid <213> Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ___ Use of <220>

Sequence(s) ___ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 ___ PatentIn 2.0 "bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ___ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001
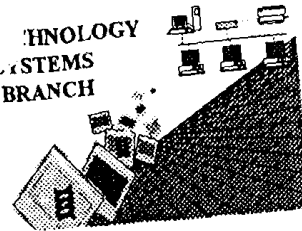
RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: **09/880,821A**

Source: **1600**

Date Processed by STIC: **5/7/2003**

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , EFS Submission **User Manual - ePAVE)**
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to:
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
   Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 04/24/2003